

REMARKS

By an Office Action dated January 13, 2003 in the file of the above-identified application, the Examiner objected to the specification of the application and also to many of the claims. Based on the amendments to the specification and claims made above, reconsideration of the merits of this patent application is respectfully requested.

First the Examiner insisted that the applicant delete references to nucleic acids encoding a *Tagetes* MinD protein, on the basis that this language recites a protein that is a non-elected species. The applicant has complied with this request by the amendments to the claims made above. The applicant still believes that the applicant is entitled to subject matter which is generic enough to cover genes encoding the *Tagetes* MinD protein.

The specification was objected to as containing an embedded hyperlink. That hyperlink has been deleted.

The specification was objected to because of the sequence identifiers which were missing from the sequences set forth on page 14, lines 7 and 8. Sequence identifiers have been added to those sequences and the substitute sequence listing is enclosed herewith for substitution for that previously in the file of this application. The paper sequence listing submitted herewith, and that submitted on computer readable form herewith, are identical.

Claims 6, 16, 19, 22, 26 and 28 were objected to for containing the phrase "selected from the group consisting of" when there is no longer a group. That informality has been corrected.

Claims 1-2, 4-5, 7, 10-12, 14-15, 17-18, 20-21, 23-24 and 27 were rejected under 35 U.S.C. §112, first paragraph on two bases. First, the Examiner argues that the claims, while enabled for an *Arabidopsis* MinD gene, do not provide an enablement for other MinD coding sequences from other plants. Secondly, the Examiner applied a rejection under §112, first paragraph, for lack of written description. The Examiner contends that the specification does not describe structural features that distinguish nucleic acids that encode MinD proteins from other nucleic acids.

First, it is noted that there has been no §112 rejection to independent Claim 3 and 8, and thus formal allowance of those claims is respectfully requested.

In response to the rejection imposed by the Examiner, the applicant both has made changes to claims above and presents arguments herewith. The applicant argues that it is entitled to claims which are broader than the specific *Arabidopsis* MinD sequence. Nevertheless, in an effort to bridge the ground with the Examiner, the applicant has amended

the independent claims above to recite a further structural limitation of the protein. In each of Claims 1, 14, 20, 24, and 27 the applicant has imported a limitation into the claim specifying two sequences of specific amino acid residues in the protein subject to these claims. These two sequences of residues are highly conserved among MinD proteins. See, for example, Figure 1, in which the two sequences are found in all MinD proteins set forth in the table. The corresponding sequences are found in the Tagetes MinD protein sequence at residues 66 to 68 and 69 to 80.

It is submitted that the claims of the application, read fairly, describe and recite a gene encoding a MinD protein which has three characteristics. One characteristic is that expression of the protein in the plant causes an alteration in size, shape and number of plasmids in the plant cells. The second characteristic is that the MinD protein encoded by the gene has an 80% sequence identity with the *Arabidopsis* MinD sequence. Thirdly, the sequence of the MinD protein is identical to twenty specific amino acids in the *Arabidopsis* MinD sequence. This provides functional, as well as structural, defining information about the MinD proteins claimed in the present patent application.

Contrary to the statement of the Examiner, the claims as constructed are not overbroad or unreasonable in breadth. They are targeted toward a specific functional gene expressed in plants that has a specific function and whose structure has been defined within tight constraints. There is nothing overbroad about these claims.

The addition to the claim language above requires a specific twenty amino acid sequence, contained within the MinD sequence claimed in the application. The sequence is highly conserved among MinD proteins, from bacteria through plants and is thus highly likely to be very important to the functionality of these proteins.

Note that there are really three MinD proteins referenced in the specification of this patent application. The *Arabidopsis* and Tagetes sequences are set forth in full, since they were available in full sequence at the time the application was filed. Note also that the rice gene (designated Os in Fig. 1) had been partially sequenced, and the protein encoded by that partial gene sequence is also presented in Fig. 1. Note that the rice protein also contains the precise motif recited in the claims above.

So, in summary, the claims are specifically limited to functional genes which have a high degree of sequence identity and which contain an exact structural motif found in all plant MinD genes yet identified at the time of filing this application. There is both function and structure thus specifically described for the claimed MinD proteins. It is well within the art ambit of ordinary skill in the art to construct, synthetically or otherwise, DNA sequences

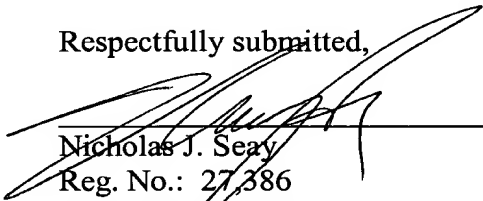
which can encode any desired protein in a plant. It is the protein that actually does something to the plant, not the DNA. Accordingly, the claim limitation which is most accurately attuned to functionality is one which is constructed at an amino acid level.

Accordingly, the applicant respectfully requests that the allowability of these claims be reconsidered.

Claim 29 has been withdrawn to render moot the objection to Claim 29.

A separate petition for extension of time is submitted herewith so that this response will be considered as timely filed.

Respectfully submitted,



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Amendments to Sequence Listing:

Please substitute the Sequence Listing submitted herewith for that previously filed in connection with this application.